

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 4, 2002, 16:16:08 ; Search time 172.18 Seconds

(without alignments) 51.241 Million cell updates/sec

Title: US-09-052-089a-6
perfect score: 293
Sequence: 1 LSCTCISDFFDHSRDVAI.....IOWFETAPSRTCPQCRIQVG 51
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL-19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8
Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB ID	Description	RESULT	1
1	293	100.0	470	11	008854	PRELIMINARY;	PRT; 470 AA.
2	296	97.6	223	11	008854	mus musculu	Q921m8
3	286	97.6	469	11	098WF2	Q9bwf2	homo sapien
4	286	97.6	470	11	09CPP4	09CPP4	mus musculu
5	272	92.8	469	4	000467	000467	homo sapien
6	244	83.3	433	13	Q9GN2	Q9ygn2	fugu rubrip
7	128	43.7	435	5	Q9SS5	Q9ss5	drosofila
8	128	43.7	455	5	Q9V8D7	Q9v8d7	drosofila
9	127	43.3	310	10	002372	082372	arabidopsis
10	127	43.3	420	4	075866	075866	homo sapien
11	125	42.7	325	10	09mgub	09mgub	arabidopsis
12	124.5	42.5	263	5	Q9SRB5	Q9sr5	arabidopsis
13	123	42.0	158	5	Q9ZS24	Q9zs24	arabidopsis
14	115	39.2	327	11	Q9DAH2	Q9dah2	mus musculu
15	39.2	349	10	Q947X9	Q947x9	oryza sativ	
16	38.9	1181	5	097260	097260	plasmidium	

RESULT	2	TRAP.
ID	0922MB	Mus musculus (Mouse).
AC	0922MB;	PRELIMINARY; PRT; 223 AA.
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX		
RN	[1]	
RP		SEQUENCE FROM N.A.
RC		STRAIN=C57BL/6J; TISSUE=EMBRYO;
RT		MEDLINE=21085660; PubMed=1127851;
RA		Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batyal S., Casavant T., Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H., Kueni P., Lewis S., Matsuo Y., Nialdo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Masilima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Sera T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
RA		"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
RT		
RL		
CC		-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR		EMBL: AK012948; BAB28567.1; -.
DR		MGI: MGI:1096377; Trap.
DR		InterPro: IPR01841; Znf_finger.
DR		Pfam: PF00097; zf-C3HC4; 1.
DR		SMART: SN00184; RING; 1.
DR		KW
RP		SEQUENCE 470 AA; 53149 MW; EBFAEC49A9F4BF2E CRC64;
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR		EMBL: BC00310; AAH00310.1; -.
DE		InterPro: IPR01841; Znf_finger.
DR		Pfam: PF00097; zf-C3HC4; 1.
DR		SMART: SN00184; RING; 1.
DR		KW
RP		SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5985B CRC64;
RC		
RA		Query Match 97.6%; Score 286; DB 4; Length 469;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR		
DR		SEQUENCE FROM N.A.
RC		
RA		Query Match 97.6%; Score 286; DB 11; Length 470;
RL		Best Local Similarity 98.0%; Pred. No. 3.2e-30;
CC		Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0

DR	Prfam; PF00097; zf-C3HC4; 1.	RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
DR	SMART; SM00184; RING; 1.	RA	Champe M., Chavaz C., Dorsett V., Farfan D., Frise E., George R.,
KW	Zinc-finger	RA	Gonzalez M., Guazin H., Li P., Liao G., Mirand A., Mungall C.J.,
SQ	SEQUENCE 469 AA; 53138 MW; 2D54ED04B84ABAEC CRC64;	RA	Nuno J., Pacleb J., Paradas V., Park S., Phouanenavong S., Wan K.,
RL	Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.	RA	Yu C., Lewis S.E., Rubin G.M., Celinker S.,
DR	EMBL; AV060610; AAL28158.1; -	DR	EMBL; AV060610; AAL28158.1; -
SEQUENCE 435 AA; 48455 MW; 0BF0AC81DD9416E CRC64;	RA	SEQUENCE 435 AA; 48455 MW; 0BF0AC81DD9416E CRC64;	
Query Match	92.8%; Score 272; DB 4; Length 469;	Best Local Similarity 96.0%; Pred. No. 2, 4e-28; Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Best Local Similarity 96.0%; Pred. No. 2, 4e-28; Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	2 SLC1CSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 51	Db	5 CTCICSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 54
RESULT	6	QYGN2	PRELIMINARY; PRT; 433 AA.
ID	QYGN2	AC	Q9YGN2; 01-MAY-1999 (TREMBlrel. 10, Created)
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)	CC	01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)	DE	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
TRAF	INTERACTING PROTEIN.	TRIP	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.	OC	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	NCBI_TaxID=1033;	OX	NCBI_TaxID=1033;
RN	[1] SEQUENCE FROM N.A.; MEDLINE=99148833; PubMed=10025966;	RP	[1] SEQUENCE FROM N.A.; MEDLINE=99148833; PubMed=10025966;
RX	Cottage A.J., Clark M., Hawker K., Umrania Y., Wheeler D., Bishop M., Elgar G.,	RA	Cottage A.J., Clark M., Hawker K., Umrania Y., Wheeler D., Bishop M., Elgar G.,
RT	"Three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes.", FEBS Lett. 443:370-374(1999).	RT	"Three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes.", FEBS Lett. 443:370-374(1999).
RL	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	CC	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMLB; AJ010317; CAA0984.1; -	DR	EMLB; AJ010317; CAA0984.1; -
DR	InterPro; IPR00841; Znf_241.	DR	InterPro; IPR00841; Znf_241.
DR	SMART; SM00184; RING; 1.	DR	SMART; SM00184; RING; 1.
KW	Zinc-finger.	OX	Zinc-finger.
SEQUENCE	433 AA; 49201 MW; A8C31AAA4216E8C2 CRC64;	RN	NCBI_TaxID=1033;
Query Match	83.3%; Score 244; DB 13; Length 433; Best Local Similarity 83.0%; Pred. No. 1, 2e-24; Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0; Oligos 0;	Best Local Similarity 83.0%; Pred. No. 1, 2e-24; Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0; Oligos 0;	
QY	4 CTCICSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 50	Db	7 CTCICSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 53
RESULT	7	Q5SS5	PRELIMINARY; PRT; 435 AA.
ID	Q5SS5	AC	Q5SS5; 01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)	DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)	DE	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	GI03577.	CG5140.	CG5140.
OS	Drosophila melanogaster (Fruit fly).	OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
RC	SEQUENCE FROM N.A.	RN	NCBI_TaxID=7227;
Query Match	43.7%; Score 128; DB 5; Length 435; Best Local Similarity 50.0%; Pred. No. 4, 2e-09; Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;	Best Local Similarity 50.0%; Pred. No. 4, 2e-09; Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;	
QY	4 CTCICSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 47	Db	6 CTCICSDFFDHSDRVDAIHCCHTFHQLCLOSFETAPSRTCPQCRCIQVG 47
RESULT	8	Q9V8D7	PRELIMINARY; PRT; 455 AA.
ID	Q9V8D7	AC	Q9V8D7; 01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)	CC	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)	DE	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	CG5140. PROTEIN.	CG5140.	CG5140. PROTEIN.
RA	Drosophila melanogaster (Fruit fly).	RA	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
RN	[1] SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.
RX	MEDLINE=2019606; PubMed=10731132;	RT	SEQUENCE FROM N.A.
RA	Adams M.D., Ceolinker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.R., Brandt R.C., Rogers Y.H.C., Blazquez R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Adril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beesn K.R., Benos P.V., Berman B.P., Bhandari D., Bolashakov S., Borikova D., Botcham M.R., Bouck J., Brokstein P., Brottier P., Burtsis K.C., Burcham D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Geibart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Guo Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavaz C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guazin H., Li P., Liao G., Mirand A., Mungall C.J., Nuno J., Pacleb J., Paradas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celinker S., Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000);
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AAC003800; AAF57730; 1; -;
 DR FlyBase; FBgn034114; CG5140;
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW ZINC-finger.
 SQ SEQUENCE 455 AA; 50726 MW; BBA74F4CAC88FD5B CRC64;
 Query Match 43.7%; Score 128; DB 5; Length 455;
 Best Local Similarity 50.0%; Pred. No. 4.4e-09; Indels 2; Gaps 1;
 Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;
 QY 4 CTCICSDFFDHSDRVAIHCGHHTPHLOCLIQWFETAPSRTCPQCR 47
 DB 6 CVCICALEFGQADSVFATVCGHMFHNLNQWLDR--SKTCPQCR 47
 RESULT 9
 ID 083372 PRELIMINARY; PRT; 310 AA.
 AC 083372;
 DT 01-NOV-1998 (TREMBREL 08, Created)
 DT 01-NOV-1998 (TREMBREL 08, Last sequence update)
 DE A12G29B40 PROTEIN.
 GN ATG29B40.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 OC NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X.; Kaul S.; Rounsley S.D.; Shea T.P.; Benito M.-I.; Town C.D.;
 RA Bowman C.L.; Barnstead M.E.; Feldblyum T.V.;
 RA Boutil C.R.; Ketchum K.A.; Lee J.J.; Ronning C.M.; Koo H.; Moffat K.S.;
 RA Cronin L.A.; Shen M.; VanAken S.E.; Umayam L.; Tallon L.J.; Gill J.E.;
 RA Adams M.D.; Carrera A.J.; Creasy T.H.; Goodman H.M.; Somerville C.R.;
 RA Copenhagen G.P.; Preuss D.; Nierman W.C.; White O.; Eisen J.A.;
 RA Salzberg S.L.; Fraser C.M.; Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AAC005496; AAC35217; 1; -;
 DR HSSP; P28990; ICHC1;
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 310 AA; 35390 MW; EEEC140115F5E2C CRC64;
 Query Match 43.3%; Score 127; DB 10; Length 310;
 Best Local Similarity 41.7%; Pred. No. 4e-09; Indels 2; Gaps 1;
 Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;
 QY 3 LCTICSDFFDHSDRVAIHCGHHTPHLOCLIQWFETAPSRTCPQCR 50
 DB 260 MC5ICLDEYEGDOLKILPCGSHYHCKC1DPMWFSQAPRRSPCVPCKOSV 346
 RESULT 11
 ID Q9N9U8 PRELIMINARY; PRT; 325 AA.
 AC Q9N9U8;
 DT 01-OCT-2000 (TREMBREL 15, Created)
 DT 01-OCT-2000 (TREMBREL 15, Last sequence update)
 DB 299 LCAICLDEYEGDOLKILPCGSHYHCKC1DPMWFSQAPRRSPCVPCKOSV 346
 SQ SEQUENCE 420 AA; 45880 MW; 572731A8E8A97FCE CRC64;
 Query Match 43.3%; Score 127; DB 4; Length 420;
 Best Local Similarity 39.6%; Pred. No. 5.5e-09; Indels 0; Gaps 0;
 Matches 19; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
 QY 3 LCTICSDFFDHSDRVAIHCGHHTPHLOCLIQWFETAPSRTCPQCR 50
 DB 299 LCAICLDEYEGDOLKILPCGSHYHCKC1DPMWFSQAPRRSPCVPCKOSV 346
 RESULT 10
 ID Q9N9U8 PRELIMINARY; PRT; 420 AA.
 AC Q9N9U8;
 DT 01-NOV-1998 (TREMBREL 08, Created)
 DT 01-NOV-1998 (TREMBREL 08, Last sequence update)
 DR IPR001841 (TREMBREL 19, Last annotation update)
 DR R31343; -;
 DR Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E.; McCready P.M.; Skowronski E.; Viswanathan V.';
 RA Burkhardt-Schultz K.; Gordon L.; Dias J.; Ramirez M.; Stilwagen S.';
 RA Phan H.; Velasco N.; Do L.; Regala W.; Terry A.; Garne J.';
 RA Danganan L.; Erler A.; Christensen M.; Amico-Keller G.; Coefield J.';
 RA Attix C.; Andreise T.; Trankheim M.; Amico-Keller G.; Coefield J.';
 RA Duarte S.; Lucas S.; Bruce R.; Thomas P.; Quan G.; Krommiller B.';
 RA Arellano A.; Saunders C.; Ow D.; Nolan M.; Trong S.; Kobayashi A.';
 RA Olsen A.S.; Carrano A.V.';
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AAC005764; AAC62428; 1; -;
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR03137; PA.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF002235; PA; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 KW Zinc-finger.
 SQ SEQUENCE 420 AA; 45880 MW; 572731A8E8A97FCE CRC64;
 Query Match 43.3%; Score 127; DB 4; Length 420;
 Best Local Similarity 39.6%; Pred. No. 5.5e-09; Indels 0; Gaps 0;
 Matches 19; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
 QY 3 LCTICSDFFDHSDRVAIHCGHHTPHLOCLIQWFETAPSRTCPQCR 50
 DB 299 LCAICLDEYEGDOLKILPCGSHYHCKC1DPMWFSQAPRRSPCVPCKOSV 346
 RESULT 11
 ID Q9N9U8 PRELIMINARY; PRT; 325 AA.
 AC Q9N9U8;
 DT 01-OCT-2000 (TREMBREL 15, Created)
 DT 01-OCT-2000 (TREMBREL 15, Last sequence update)
 DR IPR001841 (TREMBREL 19, Last annotation update)
 DR FRA14.12 PROTEIN.
 DR GN FRA14.12.
 DR OS *Arabidopsis thaliana* (Mouse-ear cress).
 DR OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 DR OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 DR OC eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 DR OC NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federerspiel N.A.; Palm C.J.; Conway A.B.; Conn L.; Hansen N.F.;
 RA Altafai H.; Araujo R.; Huizar L.; Rowley D.; Buehler E.; Dunn P.;
 RA Gonzalez A.; Kramenetskaia I.; Kim C.; Lenz C.; Li J.; Liu S.;
 RA Lueros S.; Schwartz J.; Shihom P.; Toriumi M.; Vysotskina V.S.;
 RA Walker M.; Yu G.; Ecker J.; Theologis A.; Davis R.W.;
 DR Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AC011809; AAF27102; 1; -;
 DR InterPro; IPR01664; IF.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.

DR	SMART: SM00184; RING: 1.
DR	PROSITE: PS00226; IF; UNKNOWN_1.
KW	Zinc-finger.
SEQUENCE	325 AA; 36919 MW; 837FDB7F28F2B615 CRC64;
QY	3 LCTICSDFFDHSDVAIHCGHFTFHLOCLIONFETAPSRTCPQCRIQV 50
Db	276 VCTICLEFFDDGRSIVTLPCHFDECVLEWF--VRSHVCPCLCRBL 321
RESULT	12
Q95RB5	PRELIMINARY: PRT; 263 AA.
Q95RB5	095RB5: 095RB5; 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	LE6224P.
GN	CG310916.
OS	Drosophila melanogaster (Fruit fly).
OC	Silky; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	SPRAIN-Y, CN BW SP;
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champine M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nuncio J., Parcile J., Parages V., Park S., Phoumenenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EML; AV06104; AAL29052.1; -.
DR	SEQUENCE 263 AA; 29515 MW; B98CECE994071BFF CRC64;
QY	3 LCTICSDFFDHSDVAIHCGHFTFHLOCLIONFETAPSRTCPQCRIQ 47
Db	31 LCAICNEF-RANDIIFTSRGCHVFKDCLTRWLN--SRICPQCR 74
RESULT	13
Q95ZS4	PRELIMINARY: PRT; 158 AA.
Q95ZS4	095ZS4: 095ZS4; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	EG-22E5_12 PROTEIN.
GN	EG-22E5_12 OR CG425.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	STRAIN=BERKELEY;
RA	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthy J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Arribalzaga J.-J., Andrews P., Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borkovska D., Botchan M.R., Bouck J., Brokman P., Brottcher P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablos B., Deucher A., Deng Z., Mays A.D., Dew I., Dietzsch S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Guo Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J., Houston D., Houston K.A., Hostin D., Houston T.J., Ibegwam C., Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klimmell B.E., Kodira C.D., Kraft D., Lai Z., Lasko P., Lei J., Levitsky A.A., Li J., Lin Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskiewici A., Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein-Volhard D.R., Paciob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Speer E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT
RL	Science 287:2185-2195(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RA	Murphy L., Harris D., Barrell B.;
RT	"Sequencing the distal X chromosome of Drosophila melanogaster. "
RL	Submitted (SBP-1998) to the EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RA	Bentos P.;
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC	-1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: AB003422; AAF45708.1; -.
DR	EMBL: AL01765; CAB1708.1; -.
DR	FlyBase: FBgn0026878; EG:22E5.12.
DR	InterPro: IPR00141; Znf-finger.
DR	ProDom: PF00097; zf-C3H4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;
Q95ZS4	PRELIMINARY: PRT; 158 AA.
Q95ZS4	095ZS4: 095ZS4; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	EG-22E5_12 PROTEIN.
GN	EG-22E5_12 OR CG425.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	STRAIN=BERKELEY;
RA	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthy J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Arribalzaga J.-J., Andrews P., Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borkovska D., Botchan M.R., Bouck J., Brokman P., Brottcher P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablos B., Deucher A., Deng Z., Mays A.D., Dew I., Dietzsch S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Guo Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J., Houston D., Houston K.A., Hostin D., Houston T.J., Ibegwam C., Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klimmell B.E., Kodira C.D., Kraft D., Lai Z., Lasko P., Lei J., Levitsky A.A., Li J., Lin Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskiewici A., Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein-Volhard D.R., Paciob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Speer E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC	-1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: AB003422; AAF45708.1; -.
DR	EMBL: AL01765; CAB1708.1; -.
DR	FlyBase: FBgn0026878; EG:22E5.12.
DR	InterPro: IPR00141; Znf-finger.
DR	ProDom: PF00097; zf-C3H4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;
Q95ZS4	PRELIMINARY: PRT; 158 AA.
Q95ZS4	095ZS4: 095ZS4; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	EG-22E5_12 PROTEIN.
GN	EG-22E5_12 OR CG425.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	STRAIN=BERKELEY;
RA	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthy J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Arribalzaga J.-J., Andrews P., Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borkovska D., Botchan M.R., Bouck J., Brokman P., Brottcher P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablos B., Deucher A., Deng Z., Mays A.D., Dew I., Dietzsch S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Guo Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J., Houston D., Houston K.A., Hostin D., Houston T.J., Ibegwam C., Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klimmell B.E., Kodira C.D., Kraft D., Lai Z., Lasko P., Lei J., Levitsky A.A., Li J., Lin Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskiewici A., Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein-Volhard D.R., Paciob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Speer E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC	-1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: AB003422; AAF45708.1; -.
DR	EMBL: AL01765; CAB1708.1; -.
DR	FlyBase: FBgn0026878; EG:22E5.12.
DR	InterPro: IPR00141; Znf-finger.
DR	ProDom: PF00097; zf-C3H4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;
Q95ZS4	PRELIMINARY: PRT; 158 AA.
Q95ZS4	095ZS4: 095ZS4; 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	EG-22E5_12 PROTEIN.
GN	EG-22E5_12 OR CG425.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.
OX	NCBI_TAXID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	STRAIN=BERKELEY;
RA	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Worthy J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Arribalzaga J.-J., Andrews P., Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolstakov S., Borkovska D., Botchan M.R., Bouck J., Brokman P., Brottcher P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., De Pablos B., Deucher A., Deng Z., Mays A.D., Dew I., Dietzsch S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Guo Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J., Houston D., Houston K.A., Hostin D., Houston T.J., Ibegwam C., Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klimmell B.E., Kodira C.D., Kraft D., Lai Z., Lasko P., Lei J., Levitsky A.A., Li J., Lin Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moskiewici A., Nelson S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein-Volhard D.R., Paciob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Speer E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT
RL	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
CC	-1-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL: AB003422; AAF45708.1; -.
DR	EMBL: AL01765; CAB1708.1; -.
DR	FlyBase: FBgn0026878; EG:22E5.12.
DR	InterPro: IPR00141; Znf-finger.
DR	ProDom: PF00097; zf-C3H4; 1.
DR	SMART: SM00184; RING; 1.
KW	Zinc-finger.
SQ	SEQUENCE 158 AA; 17741 MW; 21C417B040642D73 CRC64;
Q95ZS4	PRELIMINARY: PRT; 327 AA.
Q95ZS4	095ZS4: 095ZS4; 01-NOV-1999 (TREMBlrel. 17, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	SPERMATID SPECIFIC RING ZINC FINGER 1.
GN	SS2FL1.
OS	MUS musculus (Mouse).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TAXID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=257BL6J; TISSUE=TESTIS;
RX	MEDLINE=2105660; PubMed=1217851;
RA	Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y.,
RA	Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Kondo S., Yamanaka I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasikawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido T., Peso G., Quackenbush J.,
RA	Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Camincci P., de Bonaldo M.P.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
RA	Gustincich S., Hill D., Hoffmann M., Hume D.A., Kambara M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombretti P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seva T., Shibusawa Y., Storch K.-F.,
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Koitsukui S.,
RA	Hayashiwaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:605-609(2001).
CC	-!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR	EMBL; AAC005843; BAB24269.1; -.
DR	HSSP; P28990; ICHC.
DR	MGD; MGI:1341258; Ssrzf1.
DR	InterPro; IPR00051; EGF-like.
DR	InterPro; IPR00181; Znf_ring.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00184; RING_1.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW	Zinc-finger. 327 AA; 35627 MW; 5F8D34ABFE394193 CRC64;
SEQUENCE	327 AA; 35627 MW; 5F8D34ABFE394193 CRC64;
RESULT	15
Q947X9	Query Match 39.2%; Score 115; DB 11; Length 327; Best Local Similarity 35.4%; Pred. No. 1.7e-07; Matches 17; Conservative 9; Mismatches 22; Indels 0; Gaps 0; CC
AC	PRELIMINARY; PRT; 349 AA.
DT	01-DEC-2001 (TREMBREL_19, Created)
DT	01-DEC-2001 (TREMBREL_19, Last sequence update)
DE	HYPOTHETICAL 39.6 KDA PROTEIN.
GN	OSINBA0067N01_18.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Tracheophyta; Eudicotyledons; core eudicots; Rosidae; Oryzeae; Oryza.
OX	NCBI_TAXID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NIPPONBARE:
RA	la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
RA	Nascimento L., Baker J., Vil M.D., Zatavert T., Santos L., Miller B.,
RA	Kuit K., Cunnius D.M., Rodriguez S., Balia V., Shah R., Bahret A.,
RA	Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedhia N.,
RA	McCombie W.R.;
RT	"Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBA0067N01, from chromosome 3, complete sequence.";
RESULT	17
Q9M9U7	Query Match 38.9%; Score 114; DB 10; Length 1181; Best Local Similarity 36.0%; Pred. No. 8.4e-07; Matches 18; Conservative 12; Mismatches 18; Indels 2; Gaps 1; CC
AC	PRELIMINARY; PRT; 224 AA.
DT	01-OCT-2000 (TREMBREL_15, Created)
DT	01-OCT-2000 (TREMBREL_15, Last sequence update)
DE	01-DEC-2001 (TREMBREL_19, Last annotation update)
GN	F6A14_13 PROTEIN.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

RESULT 24
 095SP2 PRELIMINARY; PRT; 626 AA.
 AC 095SP2; ID 01-DEC-2001 ('TREMBLrel. 19, created)
 DT 01-DEC-2001 ('TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 ('TREMBLrel. 19, last annotation update)
 DE GH1117P.
 GN CG137.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Dirosophilidae; Dirosophila.
 OC NCBITaxonID=7227;
 RN SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongall C.J.,
 RA Munoz J., Paclay J., Paragas V., Park S., Phouanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celiker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: AY050677; AAL28225; 1.
 SEQUENCE 626 AA; 69272 MW; F881B88D51D774 EC CRC64;

RESULT 25
 09L10 PRELIMINARY; PRT; 325 AA.
 AC 09L10; ID 01-OCT-2000 ('TREMBLrel. 15, Created)
 DT 01-OCT-2000 ('TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 ('TREMBLrel. 19, last annotation update)
 DE GB|TAF27103.1
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids III; Brassicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 features of the regions of 4,504,864 bp covered by sixty p1 and tAC
 RT clones. ";
 RT DNA Res.; 7:131-135 (2000).
 RL CC -- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB024034; BAB27891; -.
 DR HSSP: P2890; 1ICHC.
 DR InterP; IPR00141; Znf_ring.
 DR PRam; PF00097; zf-CCHC4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 325 AA; 36432 MW; 694044F361053DE4 CRC64;

RESULT 26
 09L210 PRELIMINARY; PRT; 274 AA.
 AC 09L210; ID 01-OCT-2000 ('TREMBLrel. 15, Created)
 DT 01-OCT-2000 ('TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 ('TREMBLrel. 19, last annotation update)
 DE HYPOTHETICAL 31.1 KDA PROTEIN.
 GN F9G14-60.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids III; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBITaxonID=3702;
 RN [1]
 SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AL162913; CAB86029.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 274 AA; 31102 MW; 9R9B6C495A6F068 CRC64;

RESULT 27
 Q9IN35 PRELIMINARY; PRT; 230 AA.
 ID Q9IN35
 AC OPEN35;
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DE GB/AF27103.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=9162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.", DNA Res. 4:401-414(1997).
 RL DNA Res. 4:401-414(1997).
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB007644; BAB10721.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 230 AA; 26799 MW; 40335546C9C5FC72 CRC64;

Query Match 37.5%; Score 110; DB 10; Length 274;
 Best Local Similarity 38.3%; Pred. No. 6.7e-07; Indels 18; Mismatches 7; Gaps 2; RT
 Matches 18; Conservative 7; MisMatches 20; Indels 2; Gaps 1;
 DR EMBL: CAB04890.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 137 AA; 15739 MW; 6A62DC6CEB8C114 CRC64;

RESULT 28
 Q9XUMB PRELIMINARY; PRT; 489 AA.
 ID Q9XUMB
 AC Q9XUMB;
 DT 01-NOV-1999 (TREMBrel. 12, Created)
 DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE W02A11_3 PROTEIN.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

Query Match 36.9%; Score 108; DB 10; Length 230;
 Best Local Similarity 38.3%; Pred. No. 1e-06; Indels 18; Mismatches 9; Gaps 2; RT
 Matches 18; Conservative 9; MisMatches 18; Indels 2; Gaps 1;
 DR EMBL: CAB75669.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 137 AA; 15739 MW; 6A62DC6CEB8C114 CRC64;

Query Match 36.5%; Score 107; DB 4; Length 137;
 Best Local Similarity 38.3%; Pred. No. 8.5e-07; Indels 18; Mismatches 20; Gaps 2; RT
 Matches 18; Conservative 7; MisMatches 20; Indels 2; Gaps 1;
 DR EMBL: AL157474; CAB75669.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 137 AA; 15739 MW; 6A62DC6CEB8C114 CRC64;

OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RL [1]
 RP SEQUENCE FROM N.A.
 RA White S.; Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90059613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology"; Science 282:2012-2018(1998).
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: 282062; CAB04890.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 489 AA; 54865 MW; 68DFACD07BF6A540 CRC64;

RESULT 29
 Q9NSR1 PRELIMINARY; PRT; 137 AA.
 ID Q9NSR1
 AC Q9NSR1;
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DE HYPOOTHEICAL 15.7 KDA PROTEIN (LIKELY ORTHOLOG OF MOUSE ARKADIA).
 GN DKFP761D081
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TAXID=9606;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-AMIGDALE;
 RA Ottenweiler B.; Obermaier B., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAUSBERG R.; PRIMITIVE NEUROECTODERMAL;
 RA STRAUSBERG R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AL157474; CAB75669.1; -.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 137 AA; 15739 MW; 6A62DC6CEB8C114 CRC64;

Db 319 CTCQDEKEAKDVEGELRCGHFRHDCVQWML--VRKNSCPVC 360
RESULT 37
 P90990 PRELIMINARY; PRT; 425 AA.
 AC P90990; 01-MAY-1997 (TREMBREL. 03, Created)
 DT 01-DEC-2001 (TREMBREL. 03, Last sequence update)
 DE 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DT B0432.9 PROTEIN.
 GN B0432.9: Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 Rhabdiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton S., Connell M., Copsey T., Cooper J., Fulton L.,
 RA Craxton M., Dear S., Du Z., Durbin R., Evelo A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirstein J., Laikele P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopa A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprout J., Wohldmann P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Henkhaus J., Wohldmann P.;
 RT "The sequence of C. elegans cosmid B0432.9";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; U0836; AAB37893.1; -.
 DR InterPro: IPR010141; Znf_finger.
 DR Pfam: PF00097; zf-C3H4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 425 AA; 48104 MW; 375F524E5C092B2D CRC64;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Shinn P.,
 RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
 RA Hulzar L., Kremenevskaya I., Lenz C., Li J., Liu S., Luers S.,
 RA Rowley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G., Davis R.W.,
 RA Federer N.A., Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome
 T.>";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 CC !- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AC008007; AAF60531.1; -.
 DR InterPro; IPR010184; Znf_fing.
 DR Pfam; PF00097; zf-C3H4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 524 AA; 58471 MW; CFFC6AB4E39BD6FF CRC64;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE=99059613; PubMed=9851916;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.>";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Chissoe S.;
 RT "The sequence of C. elegans cosmid EBED8.>";
 RL Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RT Waterston R.;
 SQ SEQUENCE 590 AA; 67414 MW; 56EA3FEEBD7D9CEB CRC64;
 OC Query Match 35.2%; Score 105; DB 5; Length 590;
 OC Best Local Similarity 40.9%; Pred. No. 3.6e-06;
 OC Matches 18; Conservative 7; Mismatches 17; Indels 2; Gaps 1;
 OC Query Match 35.2%; Score 105; DB 5; Length 590;
 OC Best Local Similarity 44.7%; Pred. No. 6.8e-06;
 OC Matches 21; Conservative 5; Mismatches 15; Indels 6; Gaps 2;
 OC Arribalzaga thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

QY	1	LSQCTICSDFFDISRDVAIHCQCHTFHQCLQNFEPAPSRCQPCR	47	DR	HSSP; P28990; ICHC.
ID	Q9yG16	PRELIMINARY;		DR	FlyBase; FBan037944; CG6923.
DT	09yG16;			DR	InterPro; IPR001841; Znf_ring.
DT	01-MAY-2000	(TREMBrel, 13, Created)		DR	Pfam; PF00097; zf-C3H4; 1.
DT	01-MAY-2000	(TREMBrel, 13, Last sequence update)		DR	SMART; SM00184; RING; 1.
DE	CG6923	PROTEIN (LD22771P).		KW	Zinc-finger.
GN	CG6923.			SQ	SEQUENCE 1256 AA; 138666 MW; 17FA760165507E4E CRC64;
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriidae; Drosophilidae; Drosophila;				
OX	NCBL-TaxID=7227;				
RN	RN	[1]			
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BERKELEY;				
RX	MEDLINE=20196006; PubMed=10731132;			PRT;	1256 AA.
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.J., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D.,				
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,				
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beezon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,				
RA	Borkovka D., Botchan M.R., Bouc J., Brokstein P., Brottier P.,				
RA	Burtis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Fosler C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.-H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,				
RA	Pala M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,				
RA	Shue B.C., Siden-Kiamos I., Simpson M., Shupski M.P., Smith T.,				
RA	Solter E., Spradling A.C., Stapleton M., Strong R., Sun E.,				
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,				
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,				
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,				
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,				
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,				
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,				
RT	"The genome sequence of <i>Drosophila melanogaster</i> ,"				
RL	Science 287:2185-2195 (2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPRINT TM , CN BW SP;				
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,				
RA	Champe N., Chavez C., Dorsett V., Fairall D., Frise E., George R.,				
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mundall C.J.,				
RA	Nuno J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,				
RA	Yu C., Lewis S.E., Rubin G.M., Celinker S.,				
RL	Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.				
CC	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.				
DR	EMBL; A003692; AAF5493.1; -.				
DR	EMBL; AV058520; AAL13749.1; -.				

THIS PAGE BLANK (USPTO)